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<110> AVENTIS PHARMA SA
THE GOVERNMENT OF THE UNITED STATES,

<120> NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS
CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF

<130> ABCC12 GENE

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<141> 2002-03-05

<150> 60/272,759

<151> 2001-03-05

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<170> PatentIn Ver. 2.1

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tcacctctc tactttaact gtgctctcag gtggtttgcg ctgagaatgg atgtcctcat 60
gaacatcctt accttcactg tggccttggt ggtgaccctg agtttctcct ccatcagtac 120
ttcatccaaa ggctgtcat tgcatacat catccag 157

<210> 25

<211> 90

<212> DNA

<213> Homo sapiens

<400> 25

ctgagcggac tgctccaagt gtgtgtgcga acgggaacag agacgcaagc caaatccacc 60

tccgtggagc tgctcagga atacatttcg

90

<210> 26
<211> 190
<212> DNA
<213> Homo sapiens

<400> 26
acctgtgttc ctgaatgcac tcatccctc aaagtgggga cctgtcccaa ggactggccc 60
agctgtgggg agatcacctt cagagactat cagatgagat acagagacaa cccccctt 120
gttctcgaca gcctgaactt gaacatacaa agtgggcaga cagtcgggat tggtggaaga 180
acaggttccg 190

<210> 27
<211> 160
<212> DNA
<213> Homo sapiens

<400> 27
gaaagtcatt gtttaggaatg gctttgtttc gtctggtgga gccagccagt ggcacaatct 60
ttattgatga ggtggatata tgcattctca gcttgggaaga cctcagaacc aagctgactg 120
tgatcccaca ggatcctgtc ctgtttgtag gtacagtaag 160

<210> 28
<211> 79
<212> DNA
<213> Homo sapiens

<400> 28
gtacaacttg gatccctttg agagtcacac cgatgagatg ctctggcagg ttctggagag 60
aacattcatg agagacaca 79

<210> 29
<211> 114
<212> DNA
<213> Homo sapiens

<400> 29
ataatgaaac tcccagaaaa attacaggca gaagtcacag aaaatggaga aaactttctca 60
gtaggggaac gtcagctgct ttgtgtggcc cgagctcttc tccgtaattc aaag 114

<210> 30
<211> 165
<212> DNA
<213> Homo sapiens

<400> 30
atcattctcc ttgatgaagc caccgctct atggactcca agactgacac cctggttcag 60
aacaccatca aagatgcctt caagggctgc actgtgctga ccacgcccc ccgcctcaac 120
acagttctca actgcgatca cgtcctgggt atggaaaatg ggaag 165

<210> 31
<211> 289
<212> DNA
<213> Homo sapiens

<400> 31
 gtgattgagt ttgacaagcc tgaagtcctt gcagagaagc cagattctgc atttgcgatg 60
 ttactagcag cagaagtcag attgtagagg tcctggcggc tgattctaga ggaggaagag 120
 gctctgtgag atgaatagga ggagtcctca ggaggagggg ctgtcctctc cgcaggcagc 180
 cctggctctc agccctccc atccacggag tgagctgggg ctgaagttgt cccactgcc 240
 atactcagtc catgtcaccc cacttggtgg gcttgggggtt ggttctggg 289

<210> 32
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 32
 gatcctgaac acctttacaa tgcagcaatg gtggaagcct tcaaggagag ccctgctgag 60
 agagaggaag atgctggtat aatcg 85

<210> 33
 <211> 1356
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Val Gly Glu Gly Pro Tyr Leu Ile Ser Asp Leu Asp Gln Arg Gly
 1 5 10 15
 Arg Arg Arg Ser Phe Ala Glu Arg Tyr Asp Pro Ser Leu Lys Thr Met
 20 25 30
 Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp
 35 40 45
 Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met
 50 55 60
 Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu
 65 70 75 80
 Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu
 85 90 95
 Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser
 100 105 110
 His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val
 115 120 125
 Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu
 130 135 140
 Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp
 145 150 155 160
 Val Gly Ile Gly Leu Cys Ile Ala Leu Phe Ala Thr Glu Phe Thr Lys
 165 170 175
 Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile
 180 185 190

Arg	Leu	Lys	Val	Ala	Leu	Ser	Thr	Leu	Val	Phe	Glu	Asn	Leu	Val	Ser	195	200	205
Phe	Lys	Thr	Leu	Thr	His	Ile	Ser	Val	Gly	Glu	Val	Leu	Asn	Ile	Leu	210	215	220
Ser	Ser	Asp	Ser	Tyr	Ser	Leu	Phe	Glu	Ala	Ala	Leu	Phe	Cys	Pro	Leu	225	230	235
Pro	Ala	Thr	Ile	Pro	Ile	Leu	Met	Val	Phe	Cys	Ala	Ala	Tyr	Ala	Phe	245	250	255
Phe	Ile	Leu	Gly	Pro	Thr	Ala	Leu	Ile	Gly	Ile	Ser	Val	Tyr	Val	Ile	260	265	270
Phe	Ile	Pro	Val	Gln	Met	Phe	Met	Ala	Lys	Leu	Asn	Ser	Ala	Phe	Arg	275	280	285
Arg	Ser	Ala	Ile	Leu	Val	Thr	Asp	Lys	Arg	Val	Gln	Thr	Met	Asn	Glu	290	295	300
Phe	Leu	Thr	Cys	Ile	Arg	Leu	Ile	Lys	Met	Tyr	Ala	Trp	Glu	Lys	Ser	305	310	315
Phe	Thr	Asn	Thr	Ile	Gln	Asp	Ile	Arg	Arg	Arg	Glu	Arg	Lys	Leu	Leu	325	330	335
Glu	Lys	Ala	Gly	Phe	Val	Gln	Ser	Gly	Asn	Ser	Ala	Leu	Ala	Pro	Ile	340	345	350
Val	Ser	Thr	Ile	Ala	Ile	Val	Leu	Thr	Leu	Ser	Cys	His	Ile	Leu	Leu	355	360	365
Arg	Arg	Lys	Leu	Thr	Ala	Pro	Val	Ala	Phe	Ser	Val	Ile	Ala	Met	Phe	370	375	380
Asn	Val	Met	Lys	Phe	Ser	Ile	Ala	Ile	Leu	Pro	Phe	Ser	Ile	Lys	Ala	385	390	395
Met	Ala	Glu	Ala	Asn	Val	Ser	Leu	Arg	Arg	Met	Lys	Lys	Ile	Leu	Ile	405	410	415
Asp	Lys	Ser	Pro	Pro	Ser	Tyr	Ile	Thr	Gln	Pro	Glu	Asp	Pro	Asp	Thr	420	425	430
Val	Leu	Leu	Leu	Ala	Asn	Ala	Thr	Leu	Thr	Trp	Glu	His	Glu	Ala	Ser	435	440	445
Arg	Lys	Ser	Thr	Pro	Lys	Lys	Leu	Gln	Asn	Gln	Lys	Arg	His	Leu	Cys	450	455	460
Lys	Lys	Gln	Arg	Ser	Glu	Ala	Tyr	Ser	Glu	Arg	Ser	Pro	Pro	Ala	Lys	465	470	475
Gly	Ala	Thr	Gly	Pro	Glu	Glu	Gln	Ser	Asp	Ser	Leu	Lys	Ser	Val	Leu	485	490	495
His	Ser	Ile	Ser	Phe	Val	Val	Arg	Lys	Gly	Lys	Ile	Leu	Gly	Ile	Cys	500	505	510
Gly	Asn	Val	Gly	Ser	Gly	Lys	Ser	Ser	Leu	Leu	Ala	Ala	Leu	Leu	Gly			

515					520					525					
Gln	Met	Gln	Leu	Gln	Lys	Gly	Val	Val	Ala	Val	Asn	Gly	Thr	Leu	Ala
530						535					540				
Tyr	Val	Ser	Gln	Gln	Ala	Trp	Ile	Phe	His	Gly	Asn	Val	Arg	Glu	Asn
545					550					555					560
Ile	Leu	Phe	Gly	Glu	Lys	Tyr	Asp	His	Gln	Arg	Tyr	Gln	His	Thr	Val
				565					570					575	
Arg	Val	Cys	Gly	Leu	Gln	Lys	Asp	Leu	Ser	Asn	Leu	Pro	Tyr	Gly	Asp
			580					585					590		
Leu	Thr	Glu	Ile	Gly	Glu	Arg	Gly	Leu	Asn	Leu	Ser	Gly	Gly	Gln	Arg
		595					600					605			
Gln	Arg	Ile	Ser	Leu	Ala	Arg	Ala	Val	Tyr	Ser	Asp	Arg	Gln	Leu	Tyr
	610					615					620				
Leu	Leu	Asp	Asp	Pro	Leu	Ser	Ala	Val	Asp	Ala	His	Val	Gly	Lys	His
625					630					635					640
Val	Phe	Glu	Glu	Cys	Ile	Lys	Lys	Thr	Leu	Arg	Gly	Lys	Thr	Val	Val
				645					650					655	
Leu	Val	Thr	His	Gln	Leu	Gln	Phe	Leu	Glu	Ser	Cys	Asp	Glu	Val	Ile
			660					665					670		
Leu	Leu	Glu	Asp	Gly	Glu	Ile	Cys	Glu	Lys	Gly	Thr	His	Lys	Glu	Leu
		675					680					685			
Met	Glu	Glu	Arg	Gly	Arg	Tyr	Ala	Lys	Leu	Ile	His	Asn	Leu	Arg	Gly
	690					695					700				
Leu	Gln	Phe	Lys	Asp	Pro	Glu	His	Leu	Tyr	Asn	Ala	Ala	Met	Val	Glu
705					710					715					720
Ala	Phe	Lys	Glu	Ser	Pro	Ala	Glu	Arg	Glu	Glu	Asp	Ala	Val	Leu	Ala
				725					730					735	
Pro	Gly	Asn	Glu	Lys	Asp	Glu	Gly	Lys	Glu	Ser	Glu	Thr	Gly	Ser	Glu
			740					745					750		
Phe	Val	Asp	Thr	Lys	Val	Pro	Glu	His	Gln	Leu	Ile	Gln	Thr	Glu	Ser
		755					760					765			
Pro	Gln	Glu	Gly	Thr	Val	Thr	Trp	Lys	Thr	Tyr	His	Thr	Tyr	Ile	Lys
	770					775					780				
Ala	Ser	Gly	Gly	Tyr	Leu	Leu	Ser	Leu	Phe	Thr	Val	Phe	Leu	Phe	Leu
785					790					795					800
Leu	Met	Ile	Gly	Ser	Ala	Ala	Phe	Ser	Asn	Trp	Trp	Leu	Gly	Leu	Trp
				805					810					815	
Leu	Asp	Lys	Gly	Ser	Arg	Met	Thr	Cys	Gly	Pro	Gln	Gly	Asn	Arg	Thr
			820					825					830		
Met	Cys	Glu	Val	Gly	Ala	Val	Leu	Ala	Asp	Ile	Gly	Gln	His	Val	Tyr
		835					840					845			

Gln Trp Val Tyr Thr Ala Ser Met Val Phe Met Leu Val Phe Gly Val
 850 855 860
 Thr Lys Gly Phe Val Phe Thr Lys Thr Thr Leu Met Ala Ser Ser Ser
 865 870 875 880
 Leu His Asp Thr Val Phe Asp Lys Ile Leu Lys Ser Pro Met Ser Phe
 885 890 895
 Phe Asp Thr Thr Pro Thr Gly Arg Leu Met Asn Arg Phe Ser Lys Asp
 900 905 910
 Met Asp Glu Leu Asp Val Arg Leu Pro Phe His Ala Glu Asn Phe Leu
 915 920 925
 Gln Gln Phe Phe Met Val Val Phe Ile Leu Val Ile Leu Ala Ala Val
 930 935 940
 Phe Pro Ala Val Leu Leu Val Val Ala Ser Leu Ala Val Gly Phe Phe
 945 950 955 960
 Ile Leu Leu Arg Ile Phe His Arg Gly Val Gln Glu Leu Lys Lys Val
 965 970 975
 Glu Asn Val Ser Arg Ser Pro Trp Phe Thr His Ile Thr Ser Ser Met
 980 985 990
 Gln Gly Leu Gly Ile Ile His Ala Tyr Gly Lys Lys Glu Ser Cys Ile
 995 1000 1005
 Thr Tyr His Leu Leu Tyr Phe Asn Cys Ala Leu Arg Trp Phe Ala Leu
 1010 1015 1020
 Arg Met Asp Val Leu Met Asn Ile Leu Thr Phe Thr Val Ala Leu Leu
 1025 1030 1035 1040
 Val Thr Leu Ser Phe Ser Ser Ile Ser Thr Ser Ser Lys Gly Leu Ser
 1045 1050 1055
 Leu Ser Tyr Ile Ile Gln Leu Ser Gly Leu Leu Gln Val Cys Val Arg
 1060 1065 1070
 Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu Leu Leu Arg
 1075 1080 1085
 Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro Leu Lys Val
 1090 1095 1100
 Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile Thr Phe Arg
 1105 1110 1115 1120
 Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val Leu Asp Ser
 1125 1130 1135
 Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile Val Gly Arg
 1140 1145 1150
 Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val
 1155 1160 1165

Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp Ile Cys Ile
 1170 1175 1180
 Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile Pro Gln Asp
 1185 1190 1195 1200
 Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp Pro Phe Glu
 1205 1210 1215
 Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg Thr Phe Met
 1220 1225 1230
 Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala Glu Val Thr
 1235 1240 1245
 Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Val
 1250 1255 1260
 Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu Asp Glu Ala
 1265 1270 1275 1280
 Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln Asn Thr Ile
 1285 1290 1295
 Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala His Arg Leu
 1300 1305 1310
 Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu Asn Gly Lys
 1315 1320 1325
 Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys Pro Asp Ser
 1330 1335 1340
 Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu
 1345 1350 1355

<210> 34
 <211> 1359
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Val Gly Glu Gly Pro Tyr Leu Ile Ser Asp Leu Asp Gln Arg Gly
 1 5 10 15
 Arg Arg Arg Ser Phe Ala Glu Arg Tyr Asp Pro Ser Leu Lys Thr Met
 20 25 30
 Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp
 35 40 45
 Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met
 50 55 60
 Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu
 65 70 75 80
 Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu
 85 90 95

Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser
100 105 110

His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val
115 120 125

Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu
130 135 140

Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp
145 150 155 160

Val Gly Ile Gly Leu Cys Ile Ala Leu Phe Ala Thr Glu Phe Thr Lys
165 170 175

Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile
180 185 190

Arg Leu Lys Val Ala Leu Ser Thr Leu Val Phe Glu Asn Leu Val Ser
195 200 205

Phe Lys Thr Leu Thr His Ile Ser Val Gly Glu Val Leu Asn Ile Leu
210 215 220

Ser Ser Asp Ser Tyr Ser Leu Phe Glu Ala Ala Leu Phe Cys Pro Leu
225 230 235 240

Pro Ala Thr Ile Pro Ile Leu Met Val Phe Cys Ala Ala Tyr Ala Phe
245 250 255

Phe Ile Leu Gly Pro Thr Ala Leu Ile Gly Ile Ser Val Tyr Val Ile
260 265 270

Phe Ile Pro Val Gln Met Phe Met Ala Lys Leu Asn Ser Ala Phe Arg
275 280 285

Arg Ser Ala Ile Leu Val Thr Asp Lys Arg Val Gln Thr Met Asn Glu
290 295 300

Phe Leu Thr Cys Ile Arg Leu Ile Lys Met Tyr Ala Trp Glu Lys Ser
305 310 315 320

Phe Thr Asn Thr Ile Gln Asp Ile Arg Arg Arg Glu Arg Lys Leu Leu
325 330 335

Glu Lys Ala Gly Phe Val Gln Ser Gly Asn Ser Ala Leu Ala Pro Ile
340 345 350

Val Ser Thr Ile Ala Ile Val Leu Thr Leu Ser Cys His Ile Leu Leu
355 360 365

Arg Arg Lys Leu Thr Ala Pro Val Ala Phe Ser Val Ile Ala Met Phe
370 375 380

Asn Val Met Lys Phe Ser Ile Ala Ile Leu Pro Phe Ser Ile Lys Ala
385 390 395 400

Met Ala Glu Ala Asn Val Ser Leu Arg Arg Met Lys Lys Ile Leu Ile
405 410 415

Asp Lys Ser Pro Pro Ser Tyr Ile Thr Gln Pro Glu Asp Pro Asp Thr
 420 425 430
 Val Leu Leu Leu Ala Asn Ala Thr Leu Thr Trp Glu His Glu Ala Ser
 435 440 445
 Arg Lys Ser Thr Pro Lys Lys Leu Gln Asn Gln Lys Arg His Leu Cys
 450 455 460
 Lys Lys Gln Arg Ser Glu Ala Tyr Ser Glu Arg Ser Pro Pro Ala Lys
 465 470 475 480
 Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp Ser Leu Lys Ser Val Leu
 485 490 495
 His Ser Ile Ser Phe Val Val Arg Lys Gly Lys Ile Leu Gly Ile Cys
 500 505 510
 Gly Asn Val Gly Ser Gly Lys Ser Ser Leu Leu Ala Ala Leu Leu Gly
 515 520 525
 Gln Met Gln Leu Gln Lys Gly Val Val Ala Val Asn Gly Thr Leu Ala
 530 535 540
 Tyr Val Ser Gln Gln Ala Trp Ile Phe His Gly Asn Val Arg Glu Asn
 545 550 555 560
 Ile Leu Phe Gly Glu Lys Tyr Asp His Gln Arg Tyr Gln His Thr Val
 565 570 575
 Arg Val Cys Gly Leu Gln Lys Asp Leu Ser Asn Leu Pro Tyr Gly Asp
 580 585 590
 Leu Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Arg
 595 600 605
 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Leu Tyr
 610 615 620
 Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
 625 630 635 640
 Val Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
 645 650 655
 Leu Val Thr His Gln Leu Gln Phe Leu Glu Ser Cys Asp Glu Val Ile
 660 665 670
 Leu Leu Glu Asp Gly Glu Ile Cys Glu Lys Gly Thr His Lys Glu Leu
 675 680 685
 Met Glu Glu Arg Gly Arg Tyr Ala Lys Leu Ile His Asn Leu Arg Gly
 690 695 700
 Leu Gln Phe Lys Asp Pro Glu His Leu Tyr Asn Ala Ala Met Val Glu
 705 710 715 720
 Ala Phe Lys Glu Ser Pro Ala Glu Arg Glu Glu Asp Ala Gly Ile Ile
 725 730 735
 Val Leu Ala Pro Gly Asn Glu Lys Asp Glu Gly Lys Glu Ser Glu Thr

740					745					750					
Gly	Ser	Glu	Phe	Val	Asp	Thr	Lys	Val	Pro	Glu	His	Gln	Leu	Ile	Gln
		755					760					765			
Thr	Glu	Ser	Pro	Gln	Glu	Gly	Thr	Val	Thr	Trp	Lys	Thr	Tyr	His	Thr
	770					775					780				
Tyr	Ile	Lys	Ala	Ser	Gly	Gly	Tyr	Leu	Leu	Ser	Leu	Phe	Thr	Val	Phe
785					790					795					800
Leu	Phe	Leu	Leu	Met	Ile	Gly	Ser	Ala	Ala	Phe	Ser	Asn	Trp	Trp	Leu
				805					810					815	
Gly	Leu	Trp	Leu	Asp	Lys	Gly	Ser	Arg	Met	Thr	Cys	Gly	Pro	Gln	Gly
			820					825					830		
Asn	Arg	Thr	Met	Cys	Glu	Val	Gly	Ala	Val	Leu	Ala	Asp	Ile	Gly	Gln
		835					840					845			
His	Val	Tyr	Gln	Trp	Val	Tyr	Thr	Ala	Ser	Met	Val	Phe	Met	Leu	Val
	850					855					860				
Phe	Gly	Val	Thr	Lys	Gly	Phe	Val	Phe	Thr	Lys	Thr	Thr	Leu	Met	Ala
865					870					875					880
Ser	Ser	Ser	Leu	His	Asp	Thr	Val	Phe	Asp	Lys	Ile	Leu	Lys	Ser	Pro
				885					890					895	
Met	Ser	Phe	Phe	Asp	Thr	Thr	Pro	Thr	Gly	Arg	Leu	Met	Asn	Arg	Phe
			900					905					910		
Ser	Lys	Asp	Met	Asp	Glu	Leu	Asp	Val	Arg	Leu	Pro	Phe	His	Ala	Glu
		915					920					925			
Asn	Phe	Leu	Gln	Gln	Phe	Phe	Met	Val	Val	Phe	Ile	Leu	Val	Ile	Leu
	930					935					940				
Ala	Ala	Val	Phe	Pro	Ala	Val	Leu	Leu	Val	Val	Ala	Ser	Leu	Ala	Val
945					950					955					960
Gly	Phe	Phe	Ile	Leu	Leu	Arg	Ile	Phe	His	Arg	Gly	Val	Gln	Glu	Leu
				965					970					975	
Lys	Lys	Val	Glu	Asn	Val	Ser	Arg	Ser	Pro	Trp	Phe	Thr	His	Ile	Thr
			980					985					990		
Ser	Ser	Met	Gln	Gly	Leu	Gly	Ile	Ile	His	Ala	Tyr	Gly	Lys	Lys	Glu
		995					1000					1005			
Ser	Cys	Ile	Thr	Tyr	His	Leu	Leu	Tyr	Phe	Asn	Cys	Ala	Leu	Arg	Trp
	1010					1015					1020				
Phe	Ala	Leu	Arg	Met	Asp	Val	Leu	Met	Asn	Ile	Leu	Thr	Phe	Thr	Val
1025					1030					1035					1040
Ala	Leu	Leu	Val	Thr	Leu	Ser	Phe	Ser	Ser	Ile	Ser	Thr	Ser	Ser	Lys
				1045					1050					1055	
Gly	Leu	Ser	Leu	Ser	Tyr	Ile	Ile	Gln	Leu	Ser	Gly	Leu	Leu	Gln	Val
			1060					1065					1070		

Cys Val Arg Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu
1075 1080 1085

Leu Leu Arg Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro
1090 1095 1100

Leu Lys Val Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile
1105 1110 1115 1120

Thr Phe Arg Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val
1125 1130 1135

Leu Asp Ser Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile
1140 1145 1150

Val Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe
1155 1160 1165

Arg Leu Val Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp
1170 1175 1180

Ile Cys Ile Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile
1185 1190 1195 1200

Pro Gln Asp Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp
1205 1210 1215

Pro Phe Glu Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg
1220 1225 1230

Thr Phe Met Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala
1235 1240 1245

Glu Val Thr Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu
1250 1255 1260

Leu Cys Val Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu
1265 1270 1275 1280

Asp Glu Ala Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln
1285 1290 1295

Asn Thr Ile Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala
1300 1305 1310

His Arg Leu Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu
1315 1320 1325

Asn Gly Lys Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys
1330 1335 1340

Pro Asp Ser Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu
1345 1350 1355

<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 35

tccttcgccca cattttcc

18

<210> 36

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 36

attgagcacc tcgccaac

18

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 37

ttctcattca ccaaattcctc c

21

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 38

acattaaaca tggcaatcac ac

22

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 39

gtgtgattgc catgtttaat gt

22

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 40

ggagtgcatt aagaagacgc

20

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 41

cagagaggag gatgccat

18

<210> 42

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 42

cactgcaagc atggtgttc

19

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 43

ctcatcggtg tgactctca

19

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 44

tttgagagtc acaccgatga gat

23

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